

SEQUENCE LISTING

<110> HUMALYS
SINGAPORE IMMUNOLOGY NETWORK (SIGN)

<120> BINDING MOLECULES AGAINST CHIKUNGUNYA VIRUS AND USES THEREOF

<130> BRV 28 - PRIO

<160> 53

<170> PatentIn version 3.3

<210> 1

<211> 839

<212> DNA

<213> Artificial

<220>

<223> Heavy chain (DNA) of Purified 5F10F175E2

<400> 1

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atggactgga cctggagcgt cctcttcttg gtggcagcag caacaggtgc ccaactcccag      60
gtgcaactgg tgcaatctgg gtcggagttg aagaagcctg gggcctcagt gaaggtttcc      120
tgcaaggcct ctggatacac cctcaactgc tatgctatga cttgggtgcg acaggcccct      180
ggacaagggc ttgagtggat gggatggatc aacacctaca ctgggaaccc aacgtatgtc      240
cagggcttca caggacggtt tgtcttctcg ttggacacct ctgtcagcac ggcgtttctg      300
cacatcacca gcctaaaggc tgaggacact gccgtgtatt tctgtgcgag agaagggggc      360
gctcgggggt ttgactactg gggccaggga accctggtca ccgtctcctc agcctccacc      420
aagggcccat cggctcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg      480
gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca      540
ggcgccctga ccagcggcgt gcacaccttc ccggtgttcc tacagtcctc aggactctac      600
tccttcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc      660
aacgtgaatc acaagcccag caacaccaag gtggacaaga gagttgagcc caaatcttgt      720
gacaaaactc acacatgccc accgtgcca gcacctgaac tcctgggggg accgtcagtc      780
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<210> 2

<211> 260

<212> PRT

<213> Artificial

<220>

<223> Heavy chain (Protein)common to both Purified 5F10F175E2 and
Recombinant 5F10F175E2

<400> 2

Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Leu Thr Arg Tyr
 20 25 30

Ala Met Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Asn Pro Thr Tyr Val Gln Gly Phe
 50 55 60

Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Phe
 65 70 75 80

Leu His Ile Thr Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Phe Cys
 85 90 95

Ala Arg Glu Gly Gly Ala Arg Gly Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
 115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
 130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
 145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
 165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
 180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
 195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr
 210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
 225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255

Thr Pro Glu Val
260

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<210> 3
<211> 711
<212> DNA
<213> Artificial
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<220>
<223>  Light chain (DNA) of Purified 5F10F175E2
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<400>	3								
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tctgtgctga	cgcagccgcc	ctcagtgtct	ggggccccag	ggcagagggt	caccatctcc				120
tgcactggga	gcagctccaa	catcggggca	agtcatgatg	tacactggta	ccagcagctt				180
cctggaacag	ccccacaact	cctcatctat	gttaacagca	atcggccctc	aggggtccct				240
gaccgattct	ctggctccaa	gtctggcacc	tcagcctccc	tggccatcac	tgggctccag				300
gctgaggatg	aggctgatta	ttactgccag	tcctatgaca	gcaacctgag	tggttcggcg				360
gtgttcggcg	gagggacca	gttgaccgtc	ctaggtcage	ccaaggctgc	cccctcggtc				420
actctgttcc	cgccctcctc	tgaggagctt	caagccaaca	aggccacact	ggtgtgtctc				480
ataagtgact	tctaccocgg	agccgtgaca	gtggcctgga	aggcagatag	cagccccgtc				540
aaggcgggag	tggagaccac	cacaccctcc	aaacaaagca	acaacaagta	cgcggccagc				600
agctacctga	gcctgacgcc	tgagcagtg	aagtcccaca	aaagctacag	ctgccaggtc				660
acgcatgaag	ggagcacccgt	ggagaagaca	gtggccccta	cagaatgttc	a				711

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<210> 4
<211> 218
<212> PRT
<213> Artificial
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<220>
<223> Light chain (Protein) common to both Purified 5F10F175E2 and
Recombinant 5F10F175E2
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<400> 4

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Ser
20 25 30

His Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Thr Leu
 35 40 45

Leu Ile Tyr Val Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
 50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
 65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Asn
 85 90 95

Leu Ser Gly Ser Ala Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 100 105 110

Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
 115 120 125

Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
 130 135 140

Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro
 145 150 155 160

Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
 165 170 175

Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
 180 185 190

Ser His Lys Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val
 195 200 205

Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
 210 215

<210> 5
 <211> 354
 <212> DNA
 <213> Artificial

<220>
 <223> VH domain

<400> 5
 caggtgcaac tgggtgcaatc tgggtcggag ttgaagaagc ctggggcctc agtgaagggt 60
 tcctgcaagg cctctggata caccctcact cgctatgcta tgacttgggt gcgacaggcc 120

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cctggacaag ggcttgagtg gatgggatgg atcaacacct acactgggaa cccaacgtat      180
gtccaggggt tcacaggacg gtttgtcttc tcgttgagaca cctctgtcag cacggcggtt      240
ctgcacatca ccagcctaaa ggctgaggac actgccgtgt atttctgtgc gagagaaggg      300
ggcgctcggg gttttgacta ctggggccag ggaaccctgg tcaccgtctc ctca          354

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<210> 6
<211> 118
<212> PRT
<213> Artificial

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<220>
<223> VH domain

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<400> 6

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Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala
1              5              10              15

```

```

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Leu Thr Arg Tyr
          20              25              30

```

```

Ala Met Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
          35              40              45

```

```

Gly Trp Ile Asn Thr Tyr Thr Gly Asn Pro Thr Tyr Val Gln Gly Phe
          50              55              60

```

```

Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Phe
65              70              75              80

```

```

Leu His Ile Thr Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Phe Cys
          85              90              95

```

```

Ala Arg Glu Gly Gly Ala Arg Gly Phe Asp Tyr Trp Gly Gln Gly Thr
          100              105              110

```

```

Leu Val Thr Val Ser Ser
          115

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<210> 7
<211> 336
<212> DNA
<213> Artificial

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<220>
<223> VL domain

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<400> 7
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc      60

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tcttgcaactg ggagcagctc caacatcggg gcaagtcattg atgtacactg gtaccagcag 120
cttcctggaa cagccccccac actcctcatc tatgttaaca gcaatcggcc ctcagggggtc 180
cctgaccgat tctctgggtc caagtctggc acctcagcct ccttgcccat cactggggtc 240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcaacct gagggttcg 300
gcggtgttcg gcggaggagac caagttgacc gtccta 336

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```

<210> 8
<211> 112
<212> PRT
<213> Artificial

```

```

<220>
<223> VL domain

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```

<400> 8

```

```

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1          5          10          15

```

```

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Ser
          20          25          30

```

```

His Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Thr Leu
          35          40          45

```

```

Leu Ile Tyr Val Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
          50          55          60

```

```

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65          70          75          80

```

```

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Asn
          85          90          95

```

```

Leu Ser Gly Ser Ala Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
          100          105          110

```

```

<210> 9
<211> 15
<212> DNA
<213> Artificial

```

```

<220>
<223> CDRH1

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```

<400> 9
cgctatgcta tgact

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<210> 10
 <211> 5
 <212> PRT
 <213> Artificial

<220>
 <223> CDRH1

<400> 10

Arg Tyr Ala Met Thr
 1 5

<210> 11
 <211> 51
 <212> DNA
 <213> Artificial

<220>
 <223> CDRH2

<400> 11
 tggatcaaca cctacactgg gaacccaacg tatgtccagg gcttcacagg a

51

<210> 12
 <211> 17
 <212> PRT
 <213> Artificial

<220>
 <223> CDRH2

<400> 12

Trp Ile Asn Thr Tyr Thr Gly Asn Pro Thr Tyr Val Gln Gly Phe Thr
 1 5 10 15

Gly

<210> 13
 <211> 27
 <212> DNA
 <213> Artificial

<220>
 <223> CDRH3

<400> 13
 gaagggggcg ctcgggggttt tgactac

27

<210> 14
 <211> 9
 <212> PRT
 <213> Artificial

<220>
<223> CDRH3

<400> 14

Glu Gly Gly Ala Arg Gly Phe Asp Tyr
1 5

<210> 15
<211> 42
<212> DNA
<213> Artificial

<220>
<223> CDRL1

<400> 15
actgggagca gctccaacat cggggcaagt catgatgtac ac

42

<210> 16
<211> 14
<212> PRT
<213> Artificial

<220>
<223> CDRL1

<400> 16

Thr Gly Ser Ser Ser Asn Ile Gly Ala Ser His Asp Val His
1 5 10

<210> 17
<211> 21
<212> DNA
<213> Artificial

<220>
<223> CDRL2

<400> 17
gttaacagca atcggccctc a

21

<210> 18
<211> 7
<212> PRT
<213> Artificial

<220>
<223> CDRL2

<400> 18

Val Asn Ser Asn Arg Pro Ser
1 5

<210> 19
 <211> 36
 <212> DNA
 <213> Artificial

<220>
 <223> CDRL3

<400> 19
 cagtcctatg acagcaacct gagtggttcg gcggtg 36

<210> 20
 <211> 12
 <212> PRT
 <213> Artificial

<220>
 <223> CDRL3

<400> 20

Gln Ser Tyr Asp Ser Asn Leu Ser Gly Ser Ala Val
 1 5 10

<210> 21
 <211> 854
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain (DNA) of Purified 8B10F8

<400> 21
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 gtgcagctgc aggagtcggg cccaggactg gtgaagcctt cggagaccct gtccctcacc 120
 tgcactgtct ctggtgactc catcagtagt tactcctgga gctggatccg gcagccccca 180
 ggggaaggac tggagtggat tggttatata cattacactg ggagcaccaa ctacaacccc 240
 tccctcaaga gtcgactcac catatcagta gacgcgtcca agaaccagtt ctccctgaag 300
 ctgagctctg tgaccgctgc ggacacggcc gtgtattact gtgcgagaga ttgggggggg 360
 tatagcagca gctggaccta cggatatggac gtctggggcc aagggaccac ggtcaccgtc 420
 tctcagcct ccaccaaggg cccatcggtc tccccctgg caccctctc caagagcacc 480
 tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540
 gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag 600
 tctcaggac tctactcct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 660
 cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagagagtt 720
 gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gccagcacc tgaactcctg 780

gggggaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatytcccg 840
 acccctgagg tcac 854

<210> 22
 <211> 266
 <212> PRT
 <213> Artificial

<220>
 <223> Heavy chain (Protein) of common to both Purified 8B10F8 and
 Recombinant 8B10F8

<400> 22

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Ser Ser Tyr
 20 25 30

Ser Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile His Tyr Thr Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
 50 55 60

Ser Arg Leu Thr Ile Ser Val Asp Ala Ser Lys Asn Gln Phe Ser Leu
 65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Asp Trp Gly Gly Tyr Ser Ser Ser Trp Thr Tyr Gly Met Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly
 115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
 130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
 145 150 155 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
 165 170 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
 180 185 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
 195 200 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
 210 215 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
 225 230 235 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 245 250 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 260 265

<210> 23
 <211> 708
 <212> DNA
 <213> Artificial

<220>
 <223> Light chain (DNA) of Purified 8B10F8

<400> 23
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 agatgtgaca tccagatgac ccagttotcca tcttcctgt ctgcatctgt aggagacaga 120
 gtcacatca cttgccgggc gagtcagggc attagcaatt ctttagcctg gtatcagcag 180
 aaaccaggga aagcccctaa gctcctgctc tatgctgcat ccagattgga aagtggggtc 240
 ccatccaggt tcagtggcag tggatctggg acggattaca ctctcaccat cagcagcctg 300
 cagcctgaag attttgcaac ttattactgt caacagtatt atagtacccc gtacactttt 360
 ggccagggga ccaagctgga gatcaaacga actgtggctg caccatctgt cttcatcttc 420
 ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 480
 ttctatccca gagaggccaa agtacagtgg aagggtgata acgccctcca atcgggtaac 540
 tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 600
 ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660
 cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgt 708

<210> 24
 <211> 214
 <212> PRT

<213> Artificial

<220>

<223> Light chain (Protein) common to both Purified 8B10F8 and Recombinant 8B10F8

<400> 24

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Ser
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Leu
35 40 45

Tyr Ala Ala Ser Arg Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys

210

<210> 25
 <211> 369
 <212> DNA
 <213> Artificial

<220>
 <223> VH domain of Purified 8B10F8

<400> 25
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 acctgcactg tctctggtga ctccatcagt agttactcct ggagctggat ccggcagccc 120
 ccagggaagg gactggagtg gattggttat atccattaca ctgggagcac caactacaac 180
 ccctccctca agagtogact caccatatca gtagacgcgt ccaagaacca gttctccctg 240
 aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgcgag agattggggg 300
 gggatatagca gcagctggac ctacggtatg gacgtctggg gccaaaggac cacggtcacc 360
 gtctcctca 369

<210> 26
 <211> 123
 <212> PRT
 <213> Artificial

<220>
 <223> VH domain common to both Purified 8B10F8 and Recombinant 8B10F8

<400> 26

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Ser Ser Tyr
 20 25 30

Ser Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile His Tyr Thr Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
 50 55 60

Ser Arg Leu Thr Ile Ser Val Asp Ala Ser Lys Asn Gln Phe Ser Leu
 65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Asp Trp Gly Gly Tyr Ser Ser Ser Trp Thr Tyr Gly Met Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 27
 <211> 321
 <212> DNA
 <213> Artificial

<220>
 <223> VL domain

<400> 27
 gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgcc gggcgagtc gggcattagc aattctttag cctgggtatca gcagaaacca 120
 gggaaagccc ctaagctcct gctctatgct gcatccagat tggaaagtgg ggtcccatcc 180
 aggttcagtg gcagtggatc tgggacggat tacactotca ccatcagcag cctgcagcct 240
 gaagattttg caacttatta ctgtcaacag tattatagta ccccgtagac ttttggccag 300
 gggaccaagc tggagatcaa a 321

<210> 28
 <211> 107
 <212> PRT
 <213> Artificial

<220>
 <223> VL domain

<400> 28

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Ser
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Leu
 35 40 45

Tyr Ala Ala Ser Arg Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Tyr

85

90

95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 29
 <211> 15
 <212> DNA
 <213> Artificial

<220>
 <223> CDRH1

<400> 29
 agttactcct ggagc

15

<210> 30
 <211> 5
 <212> PRT
 <213> Artificial

<220>
 <223> CDRH1

<400> 30

Ser Tyr Ser Trp Ser
 1 5

<210> 31
 <211> 48
 <212> DNA
 <213> Artificial

<220>
 <223> CDRH2 of Purified 8B10F8

<400> 31
 tatatccatt aactgggag caccaactac aaccctcccc tcaagagt

48

<210> 32
 <211> 16
 <212> PRT
 <213> Artificial

<220>
 <223> CDRH2 common to both Purified 8B10F8 and Recombinant 8B10F8

<400> 32

Tyr Ile His Tyr Thr Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys Ser
 1 5 10 15

<210> 33
 <211> 45

<212> DNA
 <213> Artificial

<220>
 <223> CDRH3

<400> 33
 gattgggggg ggtatagcag cagctggacc tacggtatgg acgtc

45

<210> 34
 <211> 15
 <212> PRT
 <213> Artificial

<220>
 <223> CDRH3

<400> 34

Asp Trp Gly Gly Tyr Ser Ser Ser Trp Thr Tyr Gly Met Asp Val
 1 5 10 15

<210> 35
 <211> 33
 <212> DNA
 <213> Artificial

<220>
 <223> CDRL1

<400> 35
 cgggcgagtc agggcattag caattcttta gcc

33

<210> 36
 <211> 11
 <212> PRT
 <213> Artificial

<220>
 <223> CDRL1

<400> 36

Arg Ala Ser Gln Gly Ile Ser Asn Ser Leu Ala
 1 5 10

<210> 37
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <223> CDRL2

<400> 37
 gctgcatcca gattggaaag t

21

<210> 38
 <211> 7
 <212> PRT
 <213> Artificial

<220>
 <223> CDRL2

<400> 38

Ala Ala Ser Arg Leu Glu Ser
 1 5

<210> 39
 <211> 27
 <212> DNA
 <213> Artificial

<220>
 <223> CDRL3

<400> 39
 caacagtatt atagtacccc gtacact

27

<210> 40
 <211> 9
 <212> PRT
 <213> Artificial

<220>
 <223> CDRL3

<400> 40

Gln Gln Tyr Tyr Ser Thr Pro Tyr Thr
 1 5

<210> 41
 <211> 842
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain (DNA) Recombinant 5F10F175E2

<400> 41
 atggagacag acacactcct gctatgggta ctgctgctct gggttccagg gtcgactggc 60
 caggtgcaac tgggtgcaatc tgggtcggag ttgaagaagc ctggggcctc agtgaagggt 120
 tcctgcaagg cctctggata caccctcact cgctatgcta tgacttgggt gcgacaggcc 180
 cctggacaag ggcttgagtg gatgggatgg atcaacacct aactgggaa cccaacgtat 240
 gtccagggct tcacaggacg gtttgccttc tcgttgga cctctgtcag caccggcgttt 300
 ctgcacatca ccagcctaaa ggctgaggac actgccgtgt atttctgtgc gagagaaggg 360

```

ggcgctcggg gttttgacta ctggggccag ggaaccctgg tcaccgtctc ctcagcctcc 420
accaagggcc catcggtctt cccgctagca ccctcctcca agagcacctc tgggggcaca 480
gcgggccttg gctgcctggg caaggactac ttccccgaac cggtgacggg gtcgtggaac 540
tcaggcgccc tgaccagcgg cgtgcacacc ttccccggctg tcctacagtc ctcaggactc 600
tactccctca gcagcgtggg gaccgtgccc tccagcagct tgggcaccca gacctacatc 660
tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agagagttga gccc aaatct 720
tgtgacaaaa ctacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 780
gtcttcctct tcccccaaaa acccaaggac accctcatga tctcccgga cctgaggtc 840
ac 842

```

```

<210> 42
<211> 714
<212> DNA
<213> Artificial

```

```

<220>
<223> Light chain (DNA) of Recombinant 5F10F175E2

```

```

<400> 42
atggagacag acacactcct gctatgggta ctgctgctct gggttccagg gtcgactggc 60
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 120
tcctgcactg ggagcagctc caacatcggg gcaagtcatg atgtacactg gtaccagcag 180
cttcctggaa cagccccac actcctcatc tatgttaaca gcaatcggcc ctcaggggtc 240
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 300
caggctgagg atgaggctga ttattactgc cagtcctatg acagcaacct gagtgggtcg 360
gcggtgttcg gcggagggac caagttgacc gtcctaggtc agcccaaggc tgccccctcg 420
gtcactctgt tcccgccctc ctctgaggag cttcaagcca acaaggccac actggtgtgt 480
ctcataagtg acttctaccc gggagccgtg acagtggcct ggaaggcaga tagcagcccc 540
gtcaaggcgg gagtggagac caccacaccc tccaaacaaa gcaacaacaa gtacgcggcc 600
agcagctacc tgagcctgac gcctgagcag tggaagtccc aaaaagcta cagctgccag 660
gtcacgcatg aaggagcac cgtggagaag acagtggccc ctacagaatg ttca 714

```

```

<210> 43
<211> 857
<212> DNA
<213> Artificial

```

```

<220>
<223> Heavy chain (DNA) of Recombinant 8B10F8

```

<400> 43
atggaagacag acaacatcct gctatgggta ctgctgctct gggttcagag gtcgaactggc
60 caggtgcagc tgcaggaagtc ggcccagga ctggtgaagc cttcggagac cctgtccctc
120 acctgcactg tctctgtgta ctcactcagt agttaacctt ggaactggaat ccgacagccc
180 ccagggaagag gactggagtg gattggttat atccattaca ctgggagcac caactacaac
240 cctccctca agagccgaat caccatatca gtaagacgcgt ccaagaacca gttctccctg
300 aagctgagct ctgtgaacgc tgcggaacag gccgtgttat actgtgcgag agattggggg
360 ggtatataga gacgctggac ctacggtatg gacgtctggg gccaaaggagc cactgtcac
420 gttctctcag cctccaccaaa gggcccatcg gttctcccg tacaacctc ctccaagagc
480 acctctgggg gcaacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccggtg
540 acgtgtctgt ggaactcagg cgcctggacc agcggcgtgc acaacctccc ggtgttcta
600 cagtcctcag gactctactc cctcagcagc gttggtgaacg tgcctctccag cagcttgggc
660 acccaagacct acatctgcaa cgtgaatcac aagcccagca accccaaggt ggaacaagag
720

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 660
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 702

<210> 45
 <211> 369
 <212> DNA
 <213> Artificial

<220>
 <223> VH domain(DNA) of Recombinant 8B10F8

<400> 45
 cagggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60
 acctgcactg tctctggtga ctccatcagt agttactcct ggagctggat ccggcagccc 120
 ccagggaagg gactggagtg gattggttat atccattaca ctgggagcac caactacaac 180
 ccctccctca agagccgact caccatatca gtagacgcgt ccaagaacca gttctccctg 240
 aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgcgag agattggggg 300
 gggatatagca gcagctggac ctacggtatg gacgtctggg gccaaaggac caggtcacc 360
 gtctcctca 369

<210> 46
 <211> 48
 <212> DNA
 <213> Artificial

<220>
 <223> VH domain(DNA) of Recombinant 8B10F8

<400> 46
 tatatccatt aactgggag caccaactac aaccctccc tcaagagc 48

<210> 47
 <211> 81
 <212> DNA
 <213> Artificial

<220>
 <223> Sequence of Figure 6

<400> 47
 atggagacag acacactcct gctatgggta ctgctgctgt gggttccagg gtcgactggc 60
 ttgctagcac cctcctccaa g 81

<210> 48
 <211> 20
 <212> PRT
 <213> Artificial

<220>

<223> Mouse signal peptide (Figure 6)

<400> 48

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15

Gly Ser Thr Gly
 20

<210> 49

<211> 6

<212> PRT

<213> Artificial

<220>

<223> Human IgG1 constant region (Figure 6)

<400> 49

Leu Ala Pro Ser Ser Lys
 1 5

<210> 50

<211> 280

<212> PRT

<213> Artificial

<220>

<223> Heavy chain variable domain (VH) and a partial region of the Constant Heavy 1 (CH1) domain of 5F10F175E2 (figure 2A)

<400> 50

Met Asp Trp Thr Trp Ser Val Leu Phe Leu Val Ala Ala Ala Thr Gly
 1 5 10 15

Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys
 20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Leu
 35 40 45

Thr Arg Tyr Ala Met Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 50 55 60

Glu Trp Met Gly Trp Ile Asn Thr Tyr Thr Gly Asn Pro Thr Tyr Val
 65 70 75 80

Gln Gly Phe Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser
 85 90 95

Thr Ala Phe Leu His Ile Thr Ser Leu Lys Ala Glu Asp Thr Ala Val
 100 105 110

Tyr Phe Cys Ala Arg Glu Gly Gly Ala Arg Gly Phe Asp Tyr Trp Gly
 115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
 145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
 210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
 225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 260 265 270

Ile Ser Arg Thr Pro Glu Val Thr
 275 280

<210> 51
 <211> 237
 <212> PRT
 <213> Artificial

<220>
 <223> sequence of whole light chain of 5F10F175E2

<400> 51

Met Ala Trp Ser Pro Leu Leu Leu Thr Leu Leu Ala His Cys Thr Gly
 1 5 10 15

Ser Trp Ala Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala
20 25 30

Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile
35 40 45

Gly Ala Ser His Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala
50 55 60

Pro Thr Leu Leu Ile Tyr Val Asn Ser Asn Arg Pro Ser Gly Val Pro
65 70 75 80

Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile
85 90 95

Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr
100 105 110

Asp Ser Asn Leu Ser Gly Ser Ala Val Phe Gly Gly Gly Thr Lys Leu
115 120 125

Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro
130 135 140

Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu
145 150 155 160

Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp
165 170 175

Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln
180 185 190

Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu
195 200 205

Gln Trp Lys Ser His Lys Ser Tyr Ser Cys Gln Val Thr His Glu Gly
210 215 220

Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
225 230 235

<210> 52
<211> 285
<212> PRT

<213> Artificial

<220>

<223> Heavy chain variable domain (VH) and a partial region of the Constant Heavy 1 (CH1) domain of 8B10F8 antibody

<400> 52

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
20 25 30

Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile
35 40 45

Ser Ser Tyr Ser Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu
50 55 60

Glu Trp Ile Gly Tyr Ile His Tyr Thr Gly Ser Thr Asn Tyr Asn Pro
65 70 75 80

Ser Leu Lys Ser Arg Leu Thr Ile Ser Val Asp Ala Ser Lys Asn Gln
85 90 95

Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
100 105 110

Tyr Cys Ala Arg Asp Trp Gly Gly Tyr Ser Ser Ser Trp Thr Tyr Gly
115 120 125

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser
130 135 140

Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
145 150 155 160

Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
165 170 175

Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
180 185 190

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
195 200 205

Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile

210 215 220
 Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val
 225 230 235 240
 Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 245 250 255
 Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 260 265 270
 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 275 280 285

 <210> 53
 <211> 236
 <212> PRT
 <213> Artificial

 <220>
 <223> Whole light chain of 8B10F8 antibody

 <400> 53
 Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
 1 5 10 15
 Leu Pro Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
 20 25 30
 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
 35 40 45
 Gln Gly Ile Ser Asn Ser Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
 50 55 60
 Ala Pro Lys Leu Leu Leu Tyr Ala Ala Ser Arg Leu Glu Ser Gly Val
 65 70 75 80
 Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr
 85 90 95
 Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
 100 105 110
 Tyr Tyr Ser Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
 115 120 125

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
 130 135 140

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
 145 150 155 160

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
 165 170 175

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
 180 185 190

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
 195 200 205

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
 210 215 220

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230 235